AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claim 1 (Canceled)

2. (Original) An isolated negative-sense single stranded RNA virus (MPV) belonging to the sub-family *Pneumovirinae* of the family *Paramyxoviridae* and identifiable as phylogenetically corresponding to the genus *Metapneumovirus* by determining a nucleic acid sequence of said virus and testing it in phylogenetic tree analyses wherein maximum likelihood trees are generated using 100 bootstraps and 3 jumbles and finding it to be more closely phylogenetically corresponding to a virus isolate deposited as **I-2614** with CNCM, Paris than it is corresponding to a virus isolate of avian pneumovirus (APV) also known as turkey rhinotracheitis virus (TRTV), the aetiological agent of avian rhinotracheitis.

Claims 3 to 47 (Canceled)

48. (Previously presented) A method for detecting a mammalian metapneumovirus in a sample, wherein the method comprises:

(i) contacting a cell with the sample;

(ii) monitoring the cytopathic effect on the cell, if the cytopathic effect is identical to the cytopathic effect of hRSV or hPIV, then

(iii) testing for the presence of PIV, influenza virus, and RSV, wherein, if PIV, influenza virus, and RSV are not present in the sample, then the mammalian metapneumovirus is in the sample.

49. (Previously presented) A method for detecting a human metapneumovirus in a sample obtained from a human, wherein the method comprises:

(i) contacting a cell with the sample;

(ii) monitoring the cytopathic effect on the cell, if the cytopathic effect is identical to the cytopathic effect of hRSV or hPIV, then

(iii) testing for the presence of hPIV type 1, hPIV type 2, hPIV type 3, hPIV type 4, hRSV, influenza virus type A and influenza virus type B,

wherein, if hPIV type 1, hPIV type 2, hPIV type 3, hPIV type 4, hRSV, influenza virus type A and influenza virus type B are not present in the sample, then the human metapneumovirus is in the sample.

50. (Previously presented) A method for evaluating the risk of a mammalian metapneumovirus infection in a subject, wherein the method comprises:

(i) obtaining a sample from the subject;

(ii) contacting a cell with the sample;

(iii) monitoring the cytopathic effect on the cell, if the cytopathic effect is identical to the cytopathic effect of hRSV or hPIV, then

(iv) testing for the presence of PIV, influenza virus, and RSV,

wherein, if PIV, influenza virus, and RSV are not present in the sample, then the subject is at risk of being infected with mammalian metapneumovirus.

51. (Previously presented) A method for detecting a mammalian metapneumovirus in a sample, wherein the method comprises:

(i) contacting a cell with the sample;

(ii) monitoring the cytopathic effect on the cell, if the cytopathic effect is identical to the cytopathic effect of hRSV or hPIV, then

(iii) testing for the presence of *Paramyxovirinae*, hPIV type 1, hPIV type 2, hPIV type 3, hPIV type 4, sendai virus, simian virus type 5, New-Castle disease virus, hRSV, morbilli virus, mumps virus, Nipah virus, Hendra virus, Tupaia virus and Mapuera virus,

wherein, if *Paramyxovirinae*, hPIV type 1, hPIV type 2, hPIV type 3, hPIV type 4, sendai virus, simian virus type 5, New-Castle disease virus, hRSV, morbilli virus, mumps virus, Nipah virus, Hendra virus, Tupaia virus and Mapuera virus are not present in the sample, then the mammalian metapneumovirus is in the sample.

52. (Previously presented) The method of claim 48, 49, 50 or 51, wherein the cytopathic effect is characterized by syncytium formation and subsequent rapid internal disruption, followed by detachment of the cell from the monolayer.

53. (Previously presented) The method of claim 48, 49, 50 or 51, wherein the cell displays the cytopathic effect three passages after contacting the cell with the sample.

54. (Previously presented) The method of claim 48, 49, 50 or 51, wherein the cell is a tMK cell, a VERO cell or a A549 cell.

55. (Previously presented) The method of claim 48, 49, 50 or 51, wherein said testing step comprises detecting a nucleic acid of PIV, RSV and/or influenza virus.

56. (Previously presented) The method of claim 55, wherein said testing step comprises an RT-PCR assay at low stringency.

57. (Previously presented) The method of claim 48, 49, 50 or 51, wherein said testing step comprises detecting a protein of PIV, RSV and/or influenza virus.

58. (Previously presented) The method of claim 57, wherein said testing step comprises an immune fluorescence assay.

59. (Previously presented) The method of claim 48, 49, 50 or 51, wherein the method further comprises contacting the sample with a nucleic acid encoding an amino acid sequence that is:

(a) an amino acid sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 or 99-1 as shown in Figure 20;

(b) an amino acid sequence that is greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 or 99-1 as shown in Figure 21;

(c) an amino acid sequence that is greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 or 99-1 as shown in Figure 22;

(d) an amino acid sequence that is greater than 81% identical to the amino acid sequence of the F protein of MPV isolate 00-1 or 99-1 as shown in Figure 23;

(e) an amino acid sequence that is greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 or 99-1 as shown in Figure 24;

(f) an amino acid sequence that is greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 or 99-1 as shown in Figure 25;

(g) an amino acid sequence that is greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 or 99-1 as shown in Figure 28;

(h) an amino acid sequence that is greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 or 99-1 as shown in Figure 26; or

(i) an amino acid sequence that is greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 or 99-1 as shown in Figure 27.

60. (Previously presented) The method of claim 48, 49, 50 or 51, wherein the method further comprises contacting the sample the sample with an antibody that specifically binds to a protein that is:

(a) greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 or 99-1 as shown in Figure 20;

(b) greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 or 99-1 as shown in Figure 21;

(c) greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 or 99-1 as shown in Figure 22;

(d) greater than 81 % identical to the amino acid sequence of the F protein of MPV isolate 00-1 or 99-1 as shown in Figure 23;

(e) greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 or 99-1 as shown in Figure 24;

(f) greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 or 99-1 as shown in Figure 25;

(g) greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 or 99-1 as shown in Figure 28;

(h) greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 or 99-1 as shown in Figure 26; or

(i) greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 or 99-1 as shown in Figure 27.

61. (Previously presented) The method of claim 48, 49, 50 or 51, wherein the method further comprises contacting the sample with a first group of one or more nucleic acids that hybridize under stringent conditions to a second group of one or more nucleic acids, that encodes a protein, or fragment thereof, comprising,

(a) a sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 and 99-1 as shown in figure 20;

(b) a sequence that is greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 and 99-1 as shown in figure 21;

(c) a sequence that is greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 and 99-1 as shown in figure 22;

(d) a sequence that is greater than 81% identical to the amino acid sequence of the F protein of MPV isolate 00-1 and 99-1 as shown in figure 23:

(e) a sequence that is greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 and 99-1 as shown in figure 24;

(f) a sequence that is greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 and 99-1 as shown in figure 25;

(g) a sequence that is greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 and 99-1 as shown in figure 28;

(h) a sequence that is greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 and 99-1 as shown in figure 26; or

(i) a sequence that is greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 and 99-1 as shown in figure 27,

wherein sequence identity is determined over the entire length of the protein.

62. (new) The method of claim 48, 49, 50 or 51, wherein the method further comprises contacting the sample with one or more nucleic acids that hybridize under stringent conditions to the genome of the virus isolate deposited as I-2614 with CNCM, Paris.